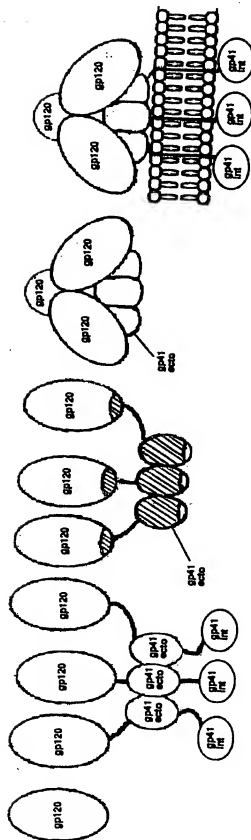


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FIGURE 1



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FIGURE 2

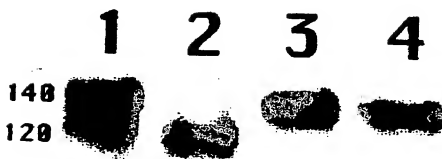
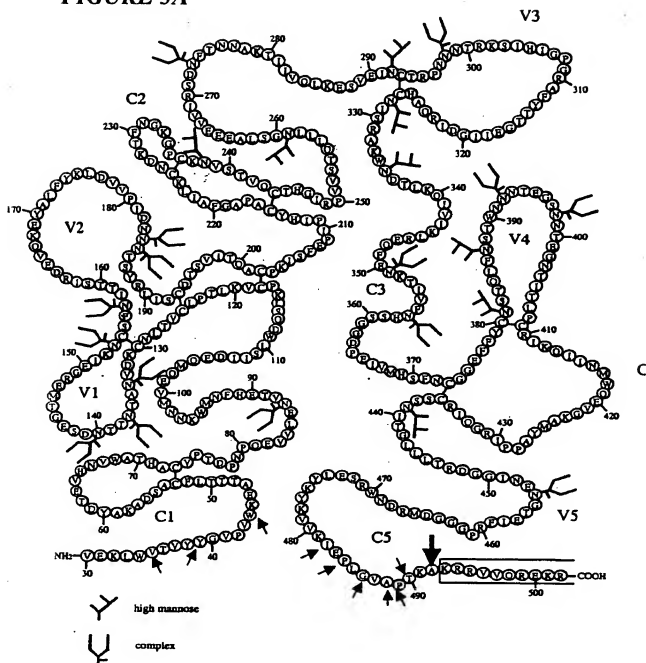
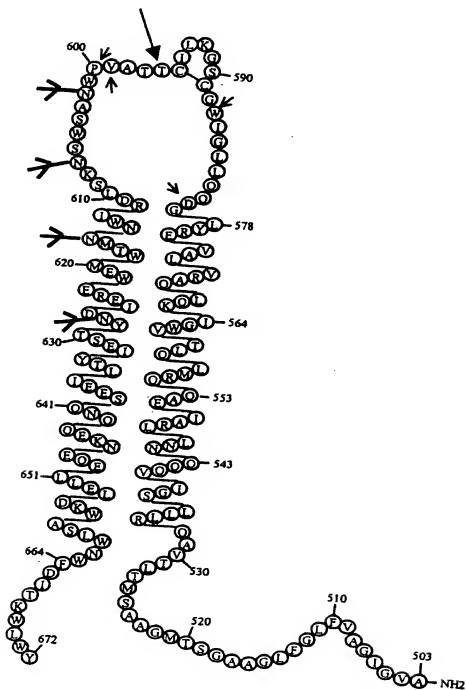


FIGURE 3A



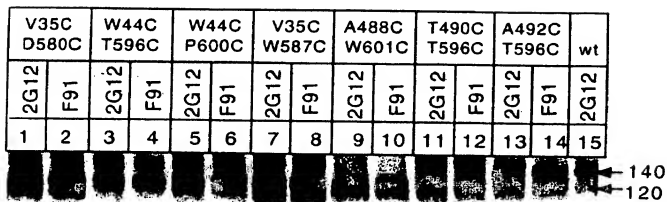
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FIGURE 3B



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FIGURE 4



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FIGURE 5

gp41

	D580C	W587C	T596C	V599C	P600C	W601C
V35C	0.45	0.40	0.35	0.30	0.40	0.30
Y39C	0.35	0.30	0.60	0.45	0.45	N.D.
W44C	0.45	0.45	0.65	0.50	0.65	0.45

gp120

C1

gp120

C5

P484C	0.35	0.30	0.45	0	0	0
G486C	0	0	0.25	0.20	0.30	0
A488C	0	0	0.05	0	0	0
P489C	0	0.10	0.30	0.15	0.05	0
T490C	0	0.15	0.55	0.25	0.25	0.10
A492C	0.05	0	0.75	0.50	0.10	0.25

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FIGURE 6A

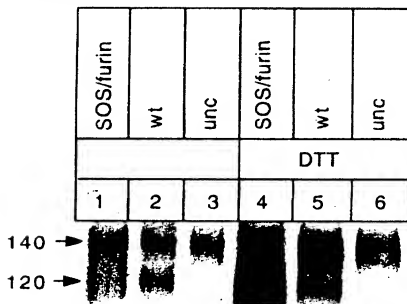


FIGURE 6B

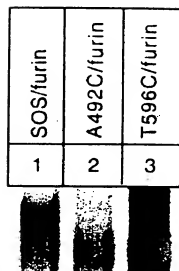
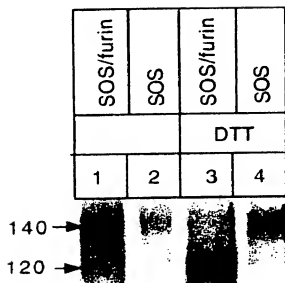


FIGURE 6C



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Serial No. 10/780,993
Filed: February 18, 2004

FIGURE 7

140	1	490, 596	
120	2	491, 596	
	3	492, 596 (SOS)	
	4	493, 596	
	5	494, 596	
	6	495, 596	
	7	496, 596	
	8	498, 596	
	9	492, 596 (SOS)	K491A
	10	492, 596 (SOS)	K493A
	11	492, 596 (SOS)	K491A, K493A
	12	44, 600; 491, 596	
	13	44, 600; 492, 596	
	14	44, 600; 493, 596	

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FIGURE 8A

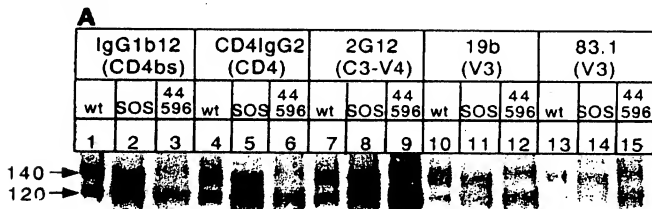


FIGURE 8B

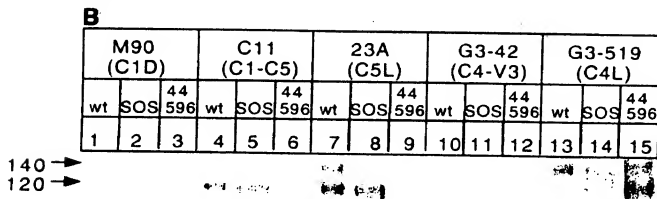
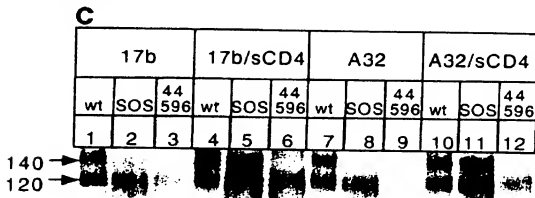


FIGURE 8C



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FIGURE 8D

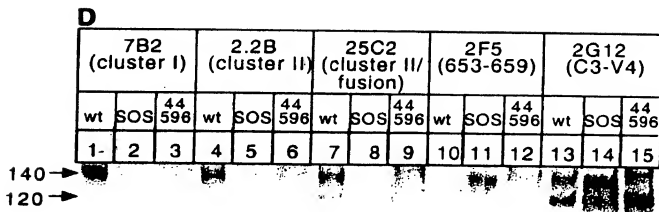
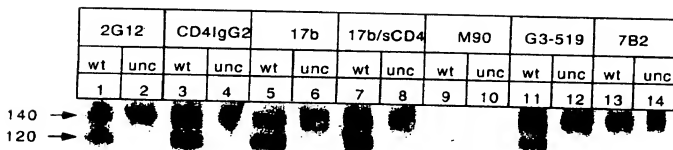


FIGURE 8E



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FIGURE 9A



FIGURE 9B

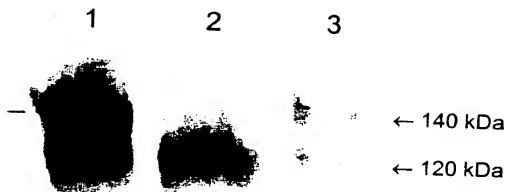
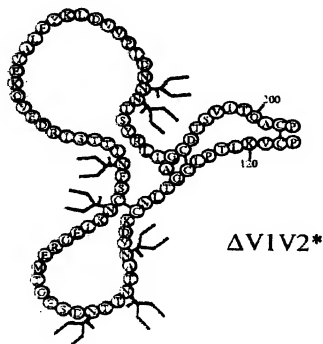
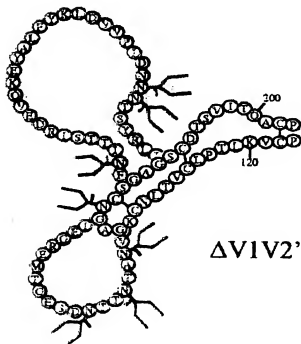
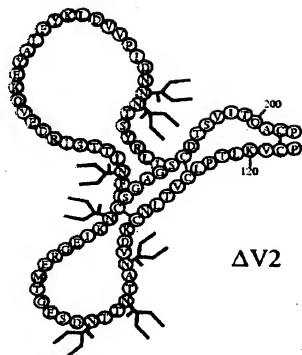
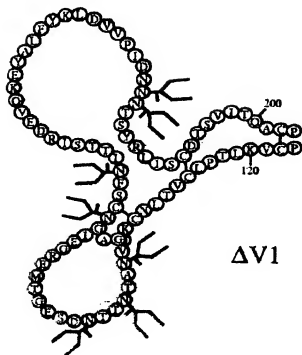


FIGURE 10

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FIGURE 11A

A

wt ΔV1V2*V3		CC ΔV1V2*V3		wt ΔV1V2*V3 N357Q N398Q		CC ΔV1V2*V3 N357Q N398Q		wt		envelope protein
2G12	F91	2G12	F91	2G12	F91	2G12	F91	F91	F91	antibody
1	2	3	4	5	6	7	8	9	10	lane

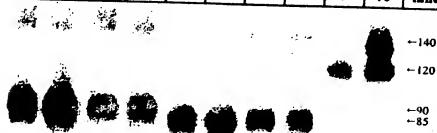
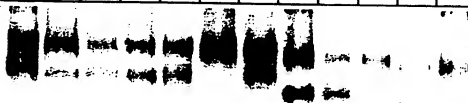


FIGURE 11B

B

wt	ΔV1		ΔV2		ΔV3		ΔV1V2'		ΔV1V2*		ΔV1V2*V3		protein
CC		CC		CC		CC		CC		CC		CC	cysteines
1	2	3	4	5	6	7	8	9	10	11	12	13	lane



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FIGURE 12A

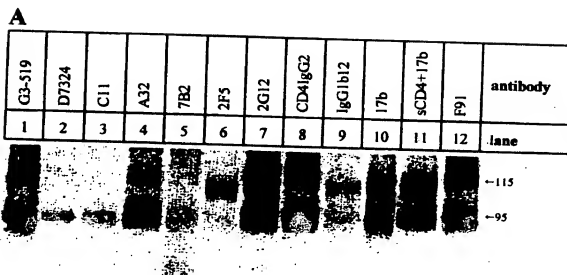
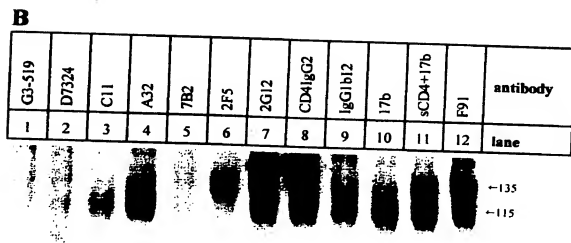


FIGURE 12B



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FIGURE 13A

HIV-1_{IR-FL} SOS gp140 (SEQ ID NO:12)

(a)
1 GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51 AGCAACCACCACCTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGTTACTTTAAAT
301 TGCAAGGATGTGAATGCTACTAATACCACTAATGATAGCGAGGGAACGAT
351 GGAGAGAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401 GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451 CCAATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501 AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATCCCATAC
551 ATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGAATGATAAGACG
601 TTCAATGGAAAAGGACCATGTAAAAATGTCAGCACAGTACAATGTACACA
651 TGGAAATTAGGCCAGTAGTATCAACTCACTGCTGTAAATGGCAGCTAG
701 CAGAAGAAGAGGTTAGTAATTAGATCTGACAAATTTACGAAACAATGCTAAA
751 ACCATAATAGTACAGCTGAAAGAATCTGTAGAATTAATTGTACAAGACC
801 CAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAGAGCATTTT
851 ATACTACAGGAGAAAAATAGGAGATATAAGACAAGCACATTGTAACATT
901 AGTAGAGCAAAATGGAATGACACTTTAAAAACAGATGTTATAAAATTAAG
951 AGAACAAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGG
1001 ACCAGAAATTTGAATGCACAGTTTTAATTGTGAAGGAGAATTTTTCTAC
1051 TGTAAATCAACACAACCTGTTTAAATAGTACTTGGAAATAATAACTGAAGG
1101 GTCAAATAACACTGAAGGAAATCTATCACACTCCCATGCAGAATAAAAC
1151 AAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCC
1201 ATCAGAGGACAAATTAGATGTTCAATCAATATTACAGGGCTGCTATTAAAC
1251 AAGAGATGGTGGTATTAAATGAGAATGGGACCGAGATCTTCAGACCTGGAG
1301 GAGGAGATATGAGGGACAATTGGAGAAGTGAATTCTATAAAATATAAGTA
1351 GTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGT
1401 GCTGCAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGT
1451 TCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACG
1501 GTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGCAACAATT
1551 GCTGAGGGCTATTGAGGCGCAACAGCGTATGTGCACTCAGCTGTGG
1601 GCATCAAGCAGCTCCAGGCAAGAGTCTGGCTGTGGAAAGATACCTAGGG
1651 GATCAACAGCTCTGGGGATTTTGGGGTGTCTCTGGAAAACCTCAATTTGCTG
1701 CACTGCTGTGCCTTGGAAATGCTAGTTGGAGTAATAATCTCTAGATAGGA
1751 TTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTAC
1801 ACAAGCGAAATATACACACTAATTGAAGAATCGCAGAACCACAAGAAAA
1851 GAATGAACAAGAAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATT
1901 GGTTTGACATAACAACTGGCTGTGGTAT

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FIGURE 13B

(SEQ ID NO:13)

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	PIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKGPKKNV	STVQCTHGIR	PVVSTQLLLN	GSLAEVEVVI	RSDNFTNNAK
280	TIIVQLKESV	EINCTRPNNN	TRKSIHIGPG	RAFYTTEGII	GDIRQAHNCI
330	SRAKWNNTLK	QIVIKLREQF	ENKTIVFNHS	SGGDPEIVMH	SFNCEGEFFY
380	CNSTQLFNST	WNNNTEGSNN	TEGNTITLPC	RIKQIINMWQ	EVGKAMYAPP
430	IRGQIRCSSN	ITGLLLTRDG	GINENGTEIF	RPGGGDMRDN	WRSEFYKYKV
480	VKIEPLGVAP	TKCRRRVVQR	EKRAVGIGAV	FLGFLGAAGS	TMGAASMTLT
530	VQARLLLSGI	VQQQNNLLRA	IEAQQRMLQL	TVWGIKQLQA	RVLAVERYLG
580	DQQLLGIWGC	SGKLCCTAV	PWNASWSNKS	LDRIWNNMTW	MEWEREIDNY
630	TSEIYTLIEE	SONQEQEKNEQ	ELLELDKWA	LWNWFIDTNW	LWY

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FIGURE 14A

HIV-1_{JR-FL} ΔV1V2* SOS gp140 (SEQ ID NO:14)

(a)
1 GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAGA
51 AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAAATTAAACCCACTCTGTGGTGCAGGATGT
301 GACACCTCAGTCATTACACAGGCCCTGTCCAAAGATATCCTTTGAGCCAAAT
351 TCCCATACATTATTGTGCCCGGCTGGTTTTGCGATTCTAAAGTGTAATG
401 ATAAGACGTTCAATGGAAAAGGACCATTGTAAAAATGTCAGCACAGTACAA
451 TGTACACATGGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTAAATGG
501 CAGCTTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACA
551 ATGCTAAAAACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGT
601 ACAAGACCCAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAG
651 AGCATTTTTATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATT
701 GTAACATTAGTAGAGCAAAATGGAATGCACTTTAAACAGATAGTTATA
751 AAATTAAGAGAACAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTC
801 AGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTGGAGGAGAAT
851 TTTTCTACTGTAATTCACACAACCTGTTTAATAGTACTTGGAAATAATAAT
901 ACTGAAGGGTCAAATAACACTGAAGGAAATACTATCACTACCTCCCATGCAG
951 AATAAAACAAATTTATAACATGTGGCAGGAAGTAGGAAAAGCAATGTATG
1001 CCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAAATTTACAGGGCTG
1051 CTATTAACAAGAGATGGTGGTATTAAATGAGAATGGGACCGAGATCTTCAG
1101 ACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAAT
1151 ATAAAGTAGTAAAAAATTGAACCAATTAGGAGTAGCACCCACCAAGTGCAAG
1201 AGAAGAGTGGTGCAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTT
1251 CTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGA
1301 CACTGACGGTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAG
1351 AACAATTTGCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCAC
1401 AGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCTGGCTGTGGAAAAGAT
1451 ACCTAGGGGATCAACAGCTCCTGGGGATTGGGGTTGCTCTGGAAAACCT
1501 ATTTGCTGCACTGCTGTGCCCTGGAATGCTAGTTGGAGTAATAAATCTCT
1551 GGATAGGATTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTG
1601 ACAATTACACAAGCGAAATATACACCCTAATTGAAGAATCGCAGAACCAA
1651 CAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTT
1701 GTGGAATTGGTTTGACATAACAACAACTGGCTGTGGTAT

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FIGURE 14B

(SEQ ID NO:15)

(b)
30 VEKLWVTYYY GVPVWKEATT TLFCASDAKA YDTEVHNVWA THACVPTDPN
80 PQEVVLENVT EHFMWKNMNM VEQMQEDIIS LWDQSLKPCV KLTPLCGAGC
130 DTSVITQACP KISFEPIPIH YCAPAGFAIL KCNDKTFNGK GPCKNVSTVQ
180 CTHGIRPVVS TQLLLNGSLA EEEVVIRSDN FTNNAKTIIV QLKESVEINC
230 TRPNNNTRKS IHIGPGRAFY TTGEIIGDIR QAHCNISRAK WNDTLKQIVI
280 KLREQFENKT IVFNHSSGGD PEIVMHSEFNC GGEFFYCNST QLENSTWNNN
330 TEGSNNTTEGN TITLPCRIKQ IINMWQEVGK AMYAPPIRGQ IRCSSNITGL
380 LLTRDGGINE NGTEIFRPGG GDMRDNWRSE LYKYKVVKIE PLGVAPTCKK
430 RRVVQREKRA VGIGAVFLGF LGAAGSTMGA ASMTLTVQAR LLLSGIVQQQ
480 NNLLRAIEAQ QRMLQLTVWG IKQLQARVLA VERYLGDOQL LGIWGCSGKL
530 ICCTAVPWNA SWSNKS LDRI WNNMTWMEWE REIDNYTSEI YTLIEESQNN
580 QEKNEQEELLE LDKWASLWNW FDI TNWLWY

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FIGURE 15A

HIV-1_{FL} ΔV3 SOS gp140 (SEQ ID NO:16)

(a)

1 GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51 AGCAACCACCACCTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAAGTAGTATTGGAAAAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAAT
301 TGCAAGGATGTGAATGCTACTAATACCACTAATGATAGCGGGGAACGAT
351 GGAGAGAGGAGAAATAAAAACTGCTCTTTTCAATATCACCACAAGCATAA
401 GAGATGAGGTGCAGAAAGAATATGCTCTTTTATAAACTTGATGTAGTA
451 CCNATAGATAATAATAATACCAGCTATAGTTGATAAGTTGTGACACCTC
501 AGTCATTACACAGGCCGTGCCAAGATATCCTTTGAGCCAATTTCCCATAC
551 ATTATTGTGCCCGGCTGGTTTTGCGATTCTAAAGTGTAATGATAAGACG
601 TTCAATGGAAAAGGNCCATGTAAAAATGTCAGCACAGTNCAATGTACACG
651 TGAATTAGGCCAGTAGTATCAACTCACTGCTGCTAAATGGCAGTCTAG
701 CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751 ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801 CAACAACAATGGAGCGGGCGATATAAGACAAGCACATTTGAACATTAGTA
851 GAGCAAAATGGAATGACACTTTAAACAGATAGTTATAAAATTAAGAGAA
901 CAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCC
951 AGAAATTGTAATGCACAGTTTAAATTGTGGAGGAGAAATTTTCTACTGTA
1001 ATTCAACACAACCTGTTTAAATAGTACTTGGAAATAAATACTGAAGGGTCA
1051 AATAACACTGAAGGAAATCTATCACACTCCCCATGCAGAATAAAACAAT
1101 TATAAATGTGGCAGGAAGTAGGAAAGCAATGTATGCCCCCTCCCATCA
1151 GAGGACAAATTAGATGTTTCATCAATATTACAGGGCTGCTATTAAACAGA
1201 GATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAGGAGG
1251 AGATATGAGGGACAAATTGGAGAAGTGAATTATATAAAATATAAGTAGTAA
1301 AAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGTGGTG
1351 CAAAGAGAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGTTCTT
1401 GGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACGGGTAC
1451 AGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAAATTTGCTG
1501 AGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCAGCTCTGGGGCAT
1551 CAAGCAGCTCCAGGCAAGAGTCTTGGCTGTGGAAAGATACCTAGGGGATC
1601 AACAGCTCCTGGGGATTGGGGTTGCTCTGGAAAACTCATTTGCTGCACT
1651 GCTGTGCCCTTGGAAATGCTAGTTGGAGTAATAAATCTCGGATAGGATTG
1701 GAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTACACAA
1751 GCGAAATATACACCCTAATTGAAGAAATCGCAGAACCAACAGAAAGAAAT
1801 GAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTT
1851 TGACATAACAAAATGGCTGTGGTAT

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FIGURE 15B

(SEQ ID NO:17)

30 VEKLWVTVYY GVPVWKEATT TLFCASDAKA YDEVHNVWA THACVPTDPN
80 PQEVVLENTV EHFNMWKNM VEQMQEDIIS LWDQSLKPCV KLTPLCVTLN
130 CKDVNATNTT NDSEGTMERG EIKNCSFNIT TSIRDEVQKE YALFYKLDVV
180 XIDNNNTSYR LISCDSVIT QACPKISFEP IPIHYCAPAG FAILKCNOKT
230 FNGKXPCKNV STXQCTHGIR PVVSTQLLN GSLAEEEVVI RSDNFTNNAK
280 TIIVQLKESV EINCTRPNNN GAGDIRQAHN NISRAKWNNT LKQIVIKLRE
330 QFENKTIVFN HSSGGDPEIV MHSFNCGGEF FYCNSTQLFN STWNNNTEGS
380 NNTEGNTITL PCRIKQIINM WQEVGKAMYA PPIRGQIRCS SNITGLLLTR
430 DGGINENGTE IFRPGGDMR DNWRSELYKY KVVKIEPLGV APTCKRRVV
480 QREKRAVGIG AVFLGELGAA GSTMGAASMT LTVQARLLS GIVQQNNLL
530 RAIEAQQRML QLTVWGIKQL QARVLAVERY LGDQQLGIW GCSGKLICCT
580 AVPWNASWSN KSLDRIWNNM TWMEWEREID NYTSEIYTLI EESQNQKEKN
630 EQELLELDKW ASLWNWFDIT KWLWY